

## SEQUENCE LISTING

<110> Holloway, James L.

<120> Human Serine Protease

<130> 99-88C1

<150> 60/167,038

<151> 1999-11-23

<150> 09/715,994

<151> 2000-11-17

<160> 4

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 807

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(807)

<400> 1

agg atc att ggg ggc cga aat gct gag cct ggc ctc ttc ccg tgg cag	48
Arg Ile Ile Gly Gly Arg Asn Ala Glu Pro Gly Leu Phe Pro Trp Gln	
1 5 10 15	
gcc ctg ata gtg gtg gag gac act tcg aga gtg cca aat gac aag tgg	96
Ala Leu Ile Val Val Glu Asp Thr Ser Arg Val Pro Asn Asp Lys Trp	
20 25 30	
ttt ggg agt ggg gcc ctg ctc tct gcg tcc tgg atc ctc aca gca gct	144
Phe Gly Ser Gly Ala Leu Leu Ser Ala Ser Trp Ile Leu Thr Ala Ala	
35 40 45	
cat gtg ctg cgc tcc cag cgt aga gac acc acg gtg ata cca gtc tcc	192
His Val Leu Arg Ser Gln Arg Arg Asp Thr Thr Val Ile Pro Val Ser	
50 55 60	

aag gag cat gtc acc gtc tac ctg ggc ttg cat gat gtg cga gac aaa Lys Glu His Val Thr Val Tyr Leu Gly Leu His Asp Val Arg Asp Lys 65 70 75 80	240
tcg ggg gca gtc aac agc tca gct gcc cga gtg gtg ctc cac cca gac Ser Gly Ala Val Asn Ser Ser Ala Ala Arg Val Val Leu His Pro Asp 85 90 95	288
ttc aac atc caa aac tac aac cac gat ata gct ctg gtg cag ctg cag Phe Asn Ile Gln Asn Tyr Asn His Asp Ile Ala Leu Val Gln Leu Gln 100 105 110	336
gag cct gtg ccc ctg gga ccc cac gtt atg cct gtc tgc ctg cca agg Glu Pro Val Pro Leu Gly Pro His Val Met Pro Val Cys Leu Pro Arg 115 120 125	384
ctt gag cct gaa ggc ccg gcc ccc cac atg ctg ggc ctg gtg gcc ggc Leu Glu Pro Glu Gly Pro Ala Pro His Met Leu Gly Leu Val Ala Gly 130 135 140	432
tgg ggc atc tcc aat ccc aat gtg aca gtg gat gag atc atc agc agt Trp Gly Ile Ser Asn Pro Asn Val Thr Val Asp Glu Ile Ile Ser Ser 145 150 155 160	480
ggc aca cgg acc ttg tca gat gtc ctg cag tat gtc aag tta ccc gtg Gly Thr Arg Thr Leu Ser Asp Val Leu Gln Tyr Val Lys Leu Pro Val 165 170 175	528
gtg cct cac gct gag tgc aaa act agc tat gag tcc cgc tcg ggc aat Val Pro His Ala Glu Cys Lys Thr Ser Tyr Glu Ser Arg Ser Gly Asn 180 185 190	576
tac agc gtc acg gag aac atg ttc tgt gct ggc tac tac gag ggc ggc Tyr Ser Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Tyr Glu Gly Gly 195 200 205	624
aaa gac acg tgc ctt gga gat agc ggt ggg gcc ttt gtc atc ttt gat Lys Asp Thr Cys Leu Gly Asp Ser Gly Gly Ala Phe Val Ile Phe Asp 210 215 220	672
gac ttg agc cag cgc tgg gtg gtg caa ggc ctg gtg tcc tgg ggg gga	720

Asp Leu Ser Gln Arg Trp Val Val Gln Gly Leu Val Ser Trp Gly Gly  
 225 230 235 240

cct gaa gaa tgc ggc agc aag cag gtc tat gga gtc tac aca aag gtc 768  
 Pro Glu Glu Cys Gly Ser Lys Gln Val Tyr Gly Val Tyr Thr Lys Val  
 245 250 255

tcc aat tac gtg gac tgg gtg tgg gag cag atg ggc tta 807  
 Ser Asn Tyr Val Asp Trp Val Trp Glu Gln Met Gly Leu  
 260 265

<210> 2

<211> 269

<212> PRT

<213> Homo sapiens

<400> 2

Arg Ile Ile Gly Gly Arg Asn Ala Glu Pro Gly Leu Phe Pro Trp Gln  
 1 5 10 15  
 Ala Leu Ile Val Val Glu Asp Thr Ser Arg Val Pro Asn Asp Lys Trp  
 20 25 30  
 Phe Gly Ser Gly Ala Leu Leu Ser Ala Ser Trp Ile Leu Thr Ala Ala  
 35 40 45  
 His Val Leu Arg Ser Gln Arg Arg Asp Thr Thr Val Ile Pro Val Ser  
 50 55 60  
 Lys Glu His Val Thr Val Tyr Leu Gly Leu His Asp Val Arg Asp Lys  
 65 70 75 80  
 Ser Gly Ala Val Asn Ser Ser Ala Ala Arg Val Val Leu His Pro Asp  
 85 90 95  
 Phe Asn Ile Gln Asn Tyr Asn His Asp Ile Ala Leu Val Gln Leu Gln  
 100 105 110  
 Glu Pro Val Pro Leu Gly Pro His Val Met Pro Val Cys Leu Pro Arg  
 115 120 125  
 Leu Glu Pro Glu Gly Pro Ala Pro His Met Leu Gly Leu Val Ala Gly  
 130 135 140  
 Trp Gly Ile Ser Asn Pro Asn Val Thr Val Asp Glu Ile Ile Ser Ser  
 145 150 155 160  
 Gly Thr Arg Thr Leu Ser Asp Val Leu Gln Tyr Val Lys Leu Pro Val  
 165 170 175  
 Val Pro His Ala Glu Cys Lys Thr Ser Tyr Glu Ser Arg Ser Gly Asn  
 180 185 190  
 Tyr Ser Val Thr Glu Asn Met Phe Cys Ala Gly Tyr Tyr Glu Gly Gly  
 195 200 205

Lys Asp Thr Cys Leu Gly Asp Ser Gly Gly Ala Phe Val Ile Phe Asp  
 210 215 220  
 Asp Leu Ser Gln Arg Trp Val Val Gln Gly Leu Val Ser Trp Gly Gly  
 225 230 235 240  
 Pro Glu Glu Cys Gly Ser Lys Gln Val Tyr Gly Val Tyr Thr Lys Val  
 245 250 255  
 Ser Asn Tyr Val Asp Trp Val Trp Glu Gln Met Gly Leu  
 260 265

<210> 3

<211> 807

<212> DNA

<213> Artificial Sequence

<220>

<223> This degenerate sequence encodes the amino acid sequence of SEQ ID NO:2.

<221> variation

<222> (1)...(807)

<223> N is any nucleotide.

<400> 3

mgnathathg	gnngnmgnaa	ygcnargccn	ggnynttttc	cntggcargc	nytnathgtn	60
gtngargaya	cnwsnmngnt	ncnnaaygay	aartggttyg	gnwsngngnc	nytnytnwsn	120
gcnwsntgga	thytnacngc	ngcncaygtn	ytnmgnwsnc	armgnmngna	yacnacngtn	180
athccngtnw	snaargarca	ygtnacngtn	tayytnngny	tncaygaygt	nmngayaar	240
wsngngcng	tnaaywsnws	ngcngcnmgn	gtngtnytn	ayccngaytt	yaayathcar	300
aaytayaayc	aygayathgc	nytngtncar	ytncargarc	cngtncnyt	nggncncay	360
gtnatgccng	tntgyytncc	nmngnytnar	ccngarggnc	cngcncnca	yatgytnngn	420
ytngtngcng	gntggggnat	hwsnaayccn	aaygtnacng	tngaygarat	hathwsnwsn	480
ggnacnmgna	cnytnwsnga	ygtnytnar	taygtnaary	tnccngtngt	nccncaygcn	540
gartgyaara	cnwsntayga	rwsnmgnwsn	ggnaaytayw	sngtnacnga	raayatgtty	600
tgycngcngt	aytaygargg	nggnaargay	acntgytyng	gngaywsngg	ngngcngntty	660
gtnathtttg	aygayytnws	ncarmngtg	gtngtncarg	gnytngtnws	ntggggnggn	720
ccngargart	gyggnwsnaa	rcargtntay	ggngtntaya	cnaargtnws	naaytaygtn	780
gaytgggtnt	gggarcarat	gggnytn				807

<210> 4

<211> 16

<212> PRT

<213> Artificial Sequence

$\langle 220 \rangle$ 

<223> Peptide linker.

<400> 4

Gly Gly Ser Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10